

SEQUENCE LISTING

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MATECZUN, ALFRED J.

<120> METHODS FOR PROTECTION AGAINST LETHAL INFECTION WITH
BACILLUS ANTHRACIS

<130> 22727-04079

<140> 09/747,521

<141> 2000-12-21

<150> 60/171,459

<151> 1999-12-22

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<170> PatentIn Ver. 3.3

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 Asn Ile Pro Ser Glu Asn Gln Tyr Phe Gln Ser Ala Ile Trp Ser Gly
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 Ile Lys Ile Gln Tyr Gln Arg Glu Asn Pro Thr Glu Lys Gly Leu Asp
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 Phe Lys Leu Tyr Trp Thr Asp Ser Gln Asn Lys Lys Glu Val Ile Ser
 165 170 175
 Ser Asp Asn Leu Gln Leu Pro Glu Leu Lys Gln Lys Ser Ser Asn Ser
 180 185 190
 Arg Lys Lys Arg Ser Thr Ser Ala Gly Pro Thr Val Pro Asp Arg Asp
 195 200 205
 Asn Asp Gly Ile Pro Asp Ser Leu Glu Val Glu Gly Tyr Thr Val Asp
 210 215 220
 Val Lys Asn Lys Arg Thr Phe Leu Ser Pro Trp Ile Ser Asn Ile His
 225 230 235 240
 Glu Lys Lys Gly Leu Thr Lys Tyr Lys Ser Ser Pro Glu Lys Trp Ser
 245 250 255
 Thr Ala Ser Asp Pro Tyr Ser Asp Phe Glu Lys Val Thr Gly Arg Ile
 260 265 270
 Asp Lys Asn Val Ser Pro Glu Ala Arg His Pro Leu Val Ala Ala Tyr
 275 280 285
 Pro Ile Val His Val Asp Met Glu Asn Ile Ile Leu Ser Lys Asn Glu
 290 295 300
 Asp Gln Ser Thr Gln Asn Thr Asp Ser Gln Thr Arg Thr Ile Ser Lys
 305 310 315 320
 Asn Thr Ser Thr Ser Arg Thr His Thr Ser Glu Val His Gly Asn Ala
 325 330 335
 Glu Val His Ala Ser Phe Phe Asp Ile Gly Gly Ser Val Ser Ala Gly
 340 345 350
 Phe Ser Asn Ser Asn Ser Ser Thr Val Ala Ile Asp His Ser Leu Ser
 355 360 365
 Leu Ala Gly Glu Arg Thr Trp Ala Glu Thr Met Gly Leu Asn Thr Ala
 370 375 380
 Asp Thr Ala Arg Leu Asn Ala Asn Ile Arg Tyr Val Asn Thr Gly Thr
 385 390 395 400

Ala Pro Ile Tyr Asn Val Leu Pro Thr Thr Ser Leu Val Leu Gly Lys
 405 410 415

Asn Gln Thr Leu Ala Thr Ile Lys Ala Lys Glu Asn Gln Leu Ser Gln
 420 425 430

Ile Leu Ala Pro Asn Asn Tyr Tyr Pro Ser Lys Asn Leu Ala Pro Ile
 435 440 445

Ala Leu Asn Ala Gln Asp Asp Phe Ser Ser Thr Pro Ile Thr Met Asn
 450 455 460

Tyr Asn Gln Phe Leu Glu Leu Glu Lys Thr Lys Gln Leu Arg Leu Asp
 465 470 475 480

Thr Asp Gln Val Tyr Gly Asn Ile Ala Thr Tyr Asn Phe Glu Asn Gly
 485 490 495

Arg Val Arg Val Asp Thr Gly Ser Asn Trp Ser Glu Val Leu Pro Gln
 500 505 510

Ile Gln Glu Thr Thr Ala Arg Ile Ile Phe Asn Gly Lys Asp Leu Asn
 515 520 525

Leu Val Glu Arg Arg Ile Ala Ala Val Asn Pro Ser Asp Pro Leu Glu
 530 535 540

Thr Thr Lys Pro Asp Met Thr Leu Lys Glu Ala Leu Lys Ile Ala Phe
 545 550 555 560

Gly Phe Asn Glu Pro Asn Gly Asn Leu Gln Tyr Gln Gly Lys Asp Ile
 565 570 575

Thr Glu Phe Asp Phe Asn Phe Asp Gln Gln Thr Ser Gln Asn Ile Lys
 580 585 590

Asn Gln Leu Ala Glu Leu Asn Ala Thr Asn Ile Tyr Thr Val Leu Asp
 595 600 605

Lys Ile Lys Leu Asn Ala Lys Met Asn Ile Leu Ile Arg Asp Lys Arg
 610 615 620

Phe His Tyr Asp Arg Asn Asn Ile Ala Val Gly Ala Asp Glu Ser Val
 625 630 635 640

Val Lys Glu Ala His Arg Glu Val Ile Asn Ser Ser Thr Glu Gly Leu
 645 650 655

Leu Leu Asn Ile Asp Lys Asp Ile Arg Lys Ile Leu Ser Gly Tyr Ile
 660 665 670

Val Glu Ile Glu Asp Thr Glu Gly Leu Lys Glu Val Ile Asn Asp Arg
 675 680 685

Tyr Asp Met Leu Asn Ile Ser Ser Leu Arg Gln Asp Gly Lys Thr Phe
 690 695 700

Ile Asp Phe Lys Lys Tyr Asn Asp Lys Leu Pro Leu Tyr Ile Ser Asn
705 710 715 720

Pro Asn Tyr Lys Val Asn Val Tyr Ala Val Thr Lys Glu Asn Thr Ile
725 730 735

Ile Asn Pro Ser Glu Asn Gly Asp Thr Ser Thr Asn Gly Ile Lys Lys
740 745 750

Ile Leu Ile Phe Ser Lys Lys Gly Tyr Glu Ile Gly
755 760

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<211> 19
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
primer

<400> 5
ctgaaaccat cacgtaaaa

19

<210> 6
<211> 26
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
primer

<400> 6
agatctgata tctaaataaa gaacga

26

<210> 7
<211> 15
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
primer

<400> 7
ctcgagacca tgggtt

15

<210> 8
<211> 15
<212> DNA
<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic primer

<400> 8

agatcttaat ggaat

15

<210> 9

<211> 2430

<212> DNA

<213> Bacillus anthracis

<220>

<221> CDS

<222> (1)..(2427)

<400> 9

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1				5					10					15		

gta	aca	gca	att	act	ttg	agt	ggt	ccc	gtc	ttt	atc	ccc	ctt	gta	cag	96
Val	Thr	Ala	Ile	Thr	Leu	Ser	Gly	Pro	Val	Phe	Ile	Pro	Leu	Val	Gln	
			20					25					30			

ggg	gcg	ggc	ggt	cat	ggt	gat	gta	ggt	atg	cac	gta	aaa	gag	aaa	gag	144
Gly	Ala	Gly	Gly	His	Gly	Asp	Val	Gly	Met	His	Val	Lys	Glu	Lys	Glu	
		35					40					45				

aaa	aat	aaa	gat	gag	aat	aag	aga	aaa	gat	gaa	gaa	cga	aat	aaa	aca	192
Lys	Asn	Lys	Asp	Glu	Asn	Lys	Arg	Lys	Asp	Glu	Glu	Arg	Asn	Lys	Thr	
	50					55						60				

cag	gaa	gag	cat	tta	aag	gaa	atc	atg	aaa	cac	att	gta	aaa	ata	gaa	240
Gln	Glu	Glu	His	Leu	Lys	Glu	Ile	Met	Lys	His	Ile	Val	Lys	Ile	Glu	
65					70				75					80		

gta	aaa	ggg	gag	gaa	gct	gtt	aaa	aaa	gag	gca	gca	gaa	aag	cta	ctt	288
Val	Lys	Gly	Glu	Glu	Ala	Val	Lys	Lys	Glu	Ala	Ala	Glu	Lys	Leu	Leu	
				85					90					95		

gag	aaa	gta	cca	tct	gat	gtt	tta	gag	atg	tat	aaa	gca	att	gga	gga	336
Glu	Lys	Val	Pro	Ser	Asp	Val	Leu	Glu	Met	Tyr	Lys	Ala	Ile	Gly	Gly	
			100					105					110			

aag	ata	tat	att	gtg	gat	ggt	gat	att	aca	aaa	cat	ata	tct	tta	gaa	384
Lys	Ile	Tyr	Ile	Val	Asp	Gly	Asp	Ile	Thr	Lys	His	Ile	Ser	Leu	Glu	
		115					120					125				

gca	tta	tct	gaa	gat	aag	aaa	aaa	ata	aaa	gac	att	tat	ggg	aaa	gat	432
Ala	Leu	Ser	Glu	Asp	Lys	Lys	Lys	Ile	Lys	Asp	Ile	Tyr	Gly	Lys	Asp	
	130					135					140					

gct	tta	tta	cat	gaa	cat	tat	gta	tat	gca	aaa	gaa	gga	tat	gaa	ccc	480
Ala	Leu	Leu	His	Glu	His	Tyr	Val	Tyr	Ala	Lys	Glu	Gly	Tyr	Glu	Pro	
145					150					155					160	

gta ctt gta atc caa tct tct gaa gat tgt gta gaa aat act gaa aag	528
Val Leu Val Ile Gln Ser Ser Glu Asp Cys Val Glu Asn Thr Glu Lys	
165 170 175	
gca ctg aac gtt tat tat gaa ata ggt aag ata tta tca agg gat att	576
Ala Leu Asn Val Tyr Tyr Glu Ile Gly Lys Ile Leu Ser Arg Asp Ile	
180 185 190	
tta agt aaa att aat caa cca tat cag aaa ttt tta gat gta tta aat	624
Leu Ser Lys Ile Asn Gln Pro Tyr Gln Lys Phe Leu Asp Val Leu Asn	
195 200 205	
acc att aaa aat gca tct gat tca gat gga caa gat ctt tta ttt act	672
Thr Ile Lys Asn Ala Ser Asp Ser Asp Gly Gln Asp Leu Leu Phe Thr	
210 215 220	
aat cag ctt aag gaa cat ccc aca gac ttt tct gta gaa ttc ttg gaa	720
Asn Gln Leu Lys Glu His Pro Thr Asp Phe Ser Val Glu Phe Leu Glu	
225 230 235 240	
caa aat agc aat gag gta caa gaa gta ttt gcg aaa gct ttt gca tat	768
Gln Asn Ser Asn Glu Val Gln Glu Val Phe Ala Lys Ala Phe Ala Tyr	
245 250 255	
tat atc gag cca cag cat cgt gat gtt tta cag ctt tat gca ccg gaa	816
Tyr Ile Glu Pro Gln His Arg Asp Val Leu Gln Leu Tyr Ala Pro Glu	
260 265 270	
gct ttt aat tac atg gat aaa ttt aac gaa caa gaa ata aat cta tcc	864
Ala Phe Asn Tyr Met Asp Lys Phe Asn Glu Gln Glu Ile Asn Leu Ser	
275 280 285	
ttg gaa gaa ctt aaa gat caa cgg atg ctg tca aga tat gaa aaa tgg	912
Leu Glu Glu Leu Lys Asp Gln Arg Met Leu Ser Arg Tyr Glu Lys Trp	
290 295 300	
gaa aag ata aaa cag cac tat caa cac tgg agc gat tct tta tct gaa	960
Glu Lys Ile Lys Gln His Tyr Gln His Trp Ser Asp Ser Leu Ser Glu	
305 310 315 320	
gaa gga aga gga ctt tta aaa aag ctg cag att cct att gag cca aag	1008
Glu Gly Arg Gly Leu Leu Lys Lys Leu Gln Ile Pro Ile Glu Pro Lys	
325 330 335	
aaa gat gac ata att cat tct tta tct caa gaa gaa aaa gag ctt cta	1056
Lys Asp Asp Ile Ile His Ser Leu Ser Gln Glu Glu Lys Glu Leu Leu	
340 345 350	
aaa aga ata caa att gat agt agt gat ttt tta tct act gag gaa aaa	1104
Lys Arg Ile Gln Ile Asp Ser Ser Asp Phe Leu Ser Thr Glu Glu Lys	
355 360 365	
gag ttt tta aaa aag cta caa att gat att cgt gat tct tta tct gaa	1152
Glu Phe Leu Lys Lys Leu Gln Ile Asp Ile Arg Asp Ser Leu Ser Glu	
370 375 380	

gaa gaa aaa gag ctt tta aat aga ata cag gtg gat agt agt aat cct Glu Glu Lys Glu Leu Leu Asn Arg Ile Gln Val Asp Ser Ser Asn Pro 385 390 395 400	1200
tta tct gaa aaa gaa aaa gag ttt tta aaa aag ctg aaa ctt gat att Leu Ser Glu Lys Glu Lys Glu Phe Leu Lys Lys Leu Lys Leu Asp Ile 405 410 415	1248
caa cca tat gat att aat caa agg ttg caa gat aca gga ggg tta att Gln Pro Tyr Asp Ile Asn Gln Arg Leu Gln Asp Thr Gly Gly Leu Ile 420 425 430	1296
gat agt ccg tca att aat ctt gat gta aga aag cag tat aaa agg gat Asp Ser Pro Ser Ile Asn Leu Asp Val Arg Lys Gln Tyr Lys Arg Asp 435 440 445	1344
att caa aat att gat gct tta tta cat caa tcc att gga agt acc ttg Ile Gln Asn Ile Asp Ala Leu Leu His Gln Ser Ile Gly Ser Thr Leu 450 455 460	1392
tac aat aaa att tat ttg tat gaa aat atg aat atc aat aac ctt aca Tyr Asn Lys Ile Tyr Leu Tyr Glu Asn Met Asn Ile Asn Asn Leu Thr 465 470 475 480	1440
gca acc cta ggt gcg gat tta gtt gat tcc act gat aat act aaa att Ala Thr Leu Gly Ala Asp Leu Val Asp Ser Thr Asp Asn Thr Lys Ile 485 490 495	1488
aat aga ggt att ttc aat gaa ttc aaa aaa aat ttc aaa tat agt att Asn Arg Gly Ile Phe Asn Glu Phe Lys Lys Asn Phe Lys Tyr Ser Ile 500 505 510	1536
tct agt aac tat atg att gtt gat ata aat gaa agg cct gca tta gat Ser Ser Asn Tyr Met Ile Val Asp Ile Asn Glu Arg Pro Ala Leu Asp 515 520 525	1584
aat gag cgt ttg aaa tgg aga atc caa tta tca cca gat act cga gca Asn Glu Arg Leu Lys Trp Arg Ile Gln Leu Ser Pro Asp Thr Arg Ala 530 535 540	1632
gga tat tta gaa aat gga aag ctt ata tta caa aga aac atc ggt ctg Gly Tyr Leu Glu Asn Gly Lys Leu Ile Leu Gln Arg Asn Ile Gly Leu 545 550 555 560	1680
gaa ata aag gat gta caa ata att aag caa tcc gaa aaa gaa tat ata Glu Ile Lys Asp Val Gln Ile Ile Lys Gln Ser Glu Lys Glu Tyr Ile 565 570 575	1728
agg att gat gcg aaa gta gtg cca aag agt aaa ata gat aca aaa att Arg Ile Asp Ala Lys Val Val Pro Lys Ser Lys Ile Asp Thr Lys Ile 580 585 590	1776
caa gaa gca cag tta aat ata aat cag gaa tgg aat aaa gca tta ggg Gln Glu Ala Gln Leu Asn Ile Asn Gln Glu Trp Asn Lys Ala Leu Gly 595 600 605	1824

tta cca aaa tat aca aag ctt att aca ttc aac gtg cat aat aga tat	1872
Leu Pro Lys Tyr Thr Lys Leu Ile Thr Phe Asn Val His Asn Arg Tyr	
610 615 620	
gca tcc aat att gta gaa agt gct tat tta ata ttg aat gaa tgg aaa	1920
Ala Ser Asn Ile Val Glu Ser Ala Tyr Leu Ile Leu Asn Glu Trp Lys	
625 630 635 640	
aat aat att caa agt gat ctt ata aaa aag gta aca aat tac tta gtt	1968
Asn Asn Ile Gln Ser Asp Leu Ile Lys Lys Val Thr Asn Tyr Leu Val	
645 650 655	
gat ggt aat gga aga ttt gtt ttt acc gat att act ctc cct aat ata	2016
Asp Gly Asn Gly Arg Phe Val Phe Thr Asp Ile Thr Leu Pro Asn Ile	
660 665 670	
gct gaa caa tat aca cat caa gat gag ata tat gag caa gtt cat tca	2064
Ala Glu Gln Tyr Thr His Gln Asp Glu Ile Tyr Glu Gln Val His Ser	
675 680 685	
aaa ggg tta tat gtt cca gaa tcc cgt tct ata tta ctc cat gga cct	2112
Lys Gly Leu Tyr Val Pro Glu Ser Arg Ser Ile Leu Leu His Gly Pro	
690 695 700	
tca aaa ggt gta gaa tta agg aat gat agt gag ggt ttt ata cac gaa	2160
Ser Lys Gly Val Glu Leu Arg Asn Asp Ser Glu Gly Phe Ile His Glu	
705 710 715 720	
ttt gga cat gct gtg gat gat tat gct gga tat cta tta gat aag aac	2208
Phe Gly His Ala Val Asp Asp Tyr Ala Gly Tyr Leu Leu Asp Lys Asn	
725 730 735	
caa tct gat tta gtt aca aat tct aaa aaa ttc att gat att ttt aag	2256
Gln Ser Asp Leu Val Thr Asn Ser Lys Lys Phe Ile Asp Ile Phe Lys	
740 745 750	
gaa gaa ggg agt aat tta act tcg tat ggg aga aca aat gaa gcg gaa	2304
Glu Glu Gly Ser Asn Leu Thr Ser Tyr Gly Arg Thr Asn Glu Ala Glu	
755 760 765	
ttt ttt gca gaa gcc ttt agg tta atg cat tct acg gac cat gct gaa	2352
Phe Phe Ala Glu Ala Phe Arg Leu Met His Ser Thr Asp His Ala Glu	
770 775 780	
cgt tta aaa gtt caa aaa aat gct ccg aaa act ttc caa ttt att aac	2400
Arg Leu Lys Val Gln Lys Asn Ala Pro Lys Thr Phe Gln Phe Ile Asn	
785 790 795 800	
gat cag att aag ttc att att aac tca taa	2430
Asp Gln Ile Lys Phe Ile Ile Asn Ser	
805	

<210> 10

<211> 809

<212> PRT

<213> Bacillus anthracis

<400> 10

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			20					25					30		
Gly	Ala	Gly	Gly	His	Gly	Asp	Val	Gly	Met	His	Val	Lys	Glu	Lys	Glu
		35					40					45			
Lys	Asn	Lys	Asp	Glu	Asn	Lys	Arg	Lys	Asp	Glu	Glu	Arg	Asn	Lys	Thr
	50					55					60				
Gln	Glu	Glu	His	Leu	Lys	Glu	Ile	Met	Lys	His	Ile	Val	Lys	Ile	Glu
65					70					75					80
Val	Lys	Gly	Glu	Glu	Ala	Val	Lys	Lys	Glu	Ala	Ala	Glu	Lys	Leu	Leu
				85					90					95	
Glu	Lys	Val	Pro	Ser	Asp	Val	Leu	Glu	Met	Tyr	Lys	Ala	Ile	Gly	Gly
			100					105					110		
Lys	Ile	Tyr	Ile	Val	Asp	Gly	Asp	Ile	Thr	Lys	His	Ile	Ser	Leu	Glu
		115					120					125			
Ala	Leu	Ser	Glu	Asp	Lys	Lys	Lys	Ile	Lys	Asp	Ile	Tyr	Gly	Lys	Asp
	130					135					140				
Ala	Leu	Leu	His	Glu	His	Tyr	Val	Tyr	Ala	Lys	Glu	Gly	Tyr	Glu	Pro
145					150					155					160
Val	Leu	Val	Ile	Gln	Ser	Ser	Glu	Asp	Cys	Val	Glu	Asn	Thr	Glu	Lys
				165					170					175	
Ala	Leu	Asn	Val	Tyr	Tyr	Glu	Ile	Gly	Lys	Ile	Leu	Ser	Arg	Asp	Ile
			180					185					190		
Leu	Ser	Lys	Ile	Asn	Gln	Pro	Tyr	Gln	Lys	Phe	Leu	Asp	Val	Leu	Asn
		195					200					205			
Thr	Ile	Lys	Asn	Ala	Ser	Asp	Ser	Asp	Gly	Gln	Asp	Leu	Leu	Phe	Thr
	210					215					220				
Asn	Gln	Leu	Lys	Glu	His	Pro	Thr	Asp	Phe	Ser	Val	Glu	Phe	Leu	Glu
225					230					235					240
Gln	Asn	Ser	Asn	Glu	Val	Gln	Glu	Val	Phe	Ala	Lys	Ala	Phe	Ala	Tyr
				245					250				255		
Tyr	Ile	Glu	Pro	Gln	His	Arg	Asp	Val	Leu	Gln	Leu	Tyr	Ala	Pro	Glu
			260					265					270		
Ala	Phe	Asn	Tyr	Met	Asp	Lys	Phe	Asn	Glu	Gln	Glu	Ile	Asn	Leu	Ser
		275					280					285			
Leu	Glu	Glu	Leu	Lys	Asp	Gln	Arg	Met	Leu	Ser	Arg	Tyr	Glu	Lys	Trp
	290					295					300				

Glu Lys Ile Lys Gln His Tyr Gln His Trp Ser Asp Ser Leu Ser Glu
 305 310 315 320
 Glu Gly Arg Gly Leu Leu Lys Lys Leu Gln Ile Pro Ile Glu Pro Lys
 325 330 335
 Lys Asp Asp Ile Ile His Ser Leu Ser Gln Glu Glu Lys Glu Leu Leu
 340 345 350
 Lys Arg Ile Gln Ile Asp Ser Ser Asp Phe Leu Ser Thr Glu Glu Lys
 355 360 365
 Glu Phe Leu Lys Lys Leu Gln Ile Asp Ile Arg Asp Ser Leu Ser Glu
 370 375 380
 Glu Glu Lys Glu Leu Leu Asn Arg Ile Gln Val Asp Ser Ser Asn Pro
 385 390 395 400
 Leu Ser Glu Lys Glu Lys Glu Phe Leu Lys Lys Leu Lys Leu Asp Ile
 405 410 415
 Gln Pro Tyr Asp Ile Asn Gln Arg Leu Gln Asp Thr Gly Gly Leu Ile
 420 425 430
 Asp Ser Pro Ser Ile Asn Leu Asp Val Arg Lys Gln Tyr Lys Arg Asp
 435 440 445
 Ile Gln Asn Ile Asp Ala Leu Leu His Gln Ser Ile Gly Ser Thr Leu
 450 455 460
 Tyr Asn Lys Ile Tyr Leu Tyr Glu Asn Met Asn Ile Asn Asn Leu Thr
 465 470 475 480
 Ala Thr Leu Gly Ala Asp Leu Val Asp Ser Thr Asp Asn Thr Lys Ile
 485 490 495
 Asn Arg Gly Ile Phe Asn Glu Phe Lys Lys Asn Phe Lys Tyr Ser Ile
 500 505 510
 Ser Ser Asn Tyr Met Ile Val Asp Ile Asn Glu Arg Pro Ala Leu Asp
 515 520 525
 Asn Glu Arg Leu Lys Trp Arg Ile Gln Leu Ser Pro Asp Thr Arg Ala
 530 535 540
 Gly Tyr Leu Glu Asn Gly Lys Leu Ile Leu Gln Arg Asn Ile Gly Leu
 545 550 555 560
 Glu Ile Lys Asp Val Gln Ile Ile Lys Gln Ser Glu Lys Glu Tyr Ile
 565 570 575
 Arg Ile Asp Ala Lys Val Val Pro Lys Ser Lys Ile Asp Thr Lys Ile
 580 585 590
 Gln Glu Ala Gln Leu Asn Ile Asn Gln Glu Trp Asn Lys Ala Leu Gly
 595 600 605

Leu Pro Lys Tyr Thr Lys Leu Ile Thr Phe Asn Val His Asn Arg Tyr
 610 615 620
 Ala Ser Asn Ile Val Glu Ser Ala Tyr Leu Ile Leu Asn Glu Trp Lys
 625 630 635 640
 Asn Asn Ile Gln Ser Asp Leu Ile Lys Lys Val Thr Asn Tyr Leu Val
 645 650 655
 Asp Gly Asn Gly Arg Phe Val Phe Thr Asp Ile Thr Leu Pro Asn Ile
 660 665 670
 Ala Glu Gln Tyr Thr His Gln Asp Glu Ile Tyr Glu Gln Val His Ser
 675 680 685
 Lys Gly Leu Tyr Val Pro Glu Ser Arg Ser Ile Leu Leu His Gly Pro
 690 695 700
 Ser Lys Gly Val Glu Leu Arg Asn Asp Ser Glu Gly Phe Ile His Glu
 705 710 715 720
 Phe Gly His Ala Val Asp Asp Tyr Ala Gly Tyr Leu Leu Asp Lys Asn
 725 730 735
 Gln Ser Asp Leu Val Thr Asn Ser Lys Lys Phe Ile Asp Ile Phe Lys
 740 745 750
 Glu Glu Gly Ser Asn Leu Thr Ser Tyr Gly Arg Thr Asn Glu Ala Glu
 755 760 765
 Phe Phe Ala Glu Ala Phe Arg Leu Met His Ser Thr Asp His Ala Glu
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 Arg Leu Lys Val Gln Lys Asn Ala Pro Lys Thr Phe Gln Phe Ile Asn
 785 790 795 800
 Asp Gln Ile Lys Phe Ile Ile Asn Ser
 805